

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- Sub  
al*
- (i) APPLICANT: Amara, Susan G  
Arriza, Jeffrey L
  - (ii) TITLE OF INVENTION: Amino Acid Transporters and Uses
  - (iii) NUMBER OF SEQUENCES: 17
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: Allegretti & Witcoff, Ltd.
    - (B) STREET: 10 South Wacker Drive, Suite 3000
    - (C) CITY: Chicago
    - (D) STATE: IL
    - (E) COUNTRY: USA
    - (F) ZIP: 60606
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER: US
    - (B) FILING DATE:
    - (C) CLASSIFICATION:
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: Noonan, Kevin E
    - (B) REGISTRATION NUMBER: 35,303
    - (C) REFERENCE/DOCKET NUMBER: 93,509
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: 312-715-1000
    - (B) TELEFAX: 312-715-1234
    - (C) TELEX: 910-221-5317

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 63 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

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(1) GENERAL INFORMATION:

- (i) APPLICANT: Amara, Susan G  
Arriza, Jeffrey L
- (ii) TITLE OF INVENTION: Amino Acid Transporters and Uses
- (iii) NUMBER OF SEQUENCES: 17
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  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/140,729
  - (B) FILING DATE: 20 OCT 1993
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Noonan, Kevin E
  - (B) REGISTRATION NUMBER: 35,303
  - (C) REFERENCE/DOCKET NUMBER: 93,509
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  - (C) TELEX: 910-221-5317

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 63 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGRGCRATG AARATGGCAG CCAGGGCYTC ATACAGGGCT GTGCCRTCCA TGTTRATGGT

60

RGC

63

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1680 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: 5'UTR  
 (B) LOCATION: 1..30

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 31..1626

- (ix) FEATURE:  
 (A) NAME/KEY: 3'UTR  
 (B) LOCATION: 1626..1680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CACCTCTAGC TCGGAGCGGC GTGTAGCGCC ATG GAG AAG AGC AAC GAG ACC AAC	54
Met Glu Lys Ser Asn Glu Thr Asn	
1 5	
GGC TAC CTT GAC AGC GCT CAG GCG GGG CCT GCG GCC GGG CCC GGA GCT	102
Gly Tyr Leu Asp Ser Ala Gln Ala Gly Pro Ala Ala Gly Pro Gly Ala	
10 15 20	
CCG GGG ACC GCG GCG GGA CGC GCA CGG CGT TGC GCG CGC TTC CTG CGG	150
Pro Gly Thr Ala Ala Gly Arg Ala Arg Arg Cys Ala Arg Phe Leu Arg	
25 30 35 40	
CGC CAA GCG CTG GTG CTG CTC ACC GTG TCC GGG GTG CTG GCG GGC GCG	198
Arg Gln Ala Leu Val Leu Leu Thr Val Ser Gly Val Leu Ala Gly Ala	
45 50 55	
GGC CTG GGC GCG GCG TTG CGC GGG CTC AGC CTG AGC CGC ACG CAG GTC	246
Gly Leu Gly Ala Ala Leu Arg Gly Leu Ser Leu Ser Arg Thr Gln Val	
60 65 70	
ACC TAC CTG GCC TTC CCC GGC GAG ATG CTG CTC CGC ATG CTG CGC ATG	294
Thr Tyr Leu Ala Phe Pro Gly Glu Met Leu Leu Arg Met Leu Arg Met	
75 80 85	
ATC ATC CTG CCG CTG GTG GTC TGC AGC CTG GTG TCG GGC GCC GCC TCG	342
Ile Ile Leu Pro Leu Val Val Cys Ser Leu Val Ser Gly Ala Ala Ser	
90 95 100	
CTC GAT GCC AGC TGC CTC GGG CGT CTG GGC GGC ATC CGT GTC GCC TAC	390
Leu Asp Ala Ser Cys Leu Gly Arg Leu Gly Gly Ile Arg Val Ala Tyr	
105 110 115 120	
TTT GGC CTC ACC ACA CTG AGT GCC TCG GCG CTC GCC GTG GCC TTG GCG	438
Phe Gly Leu Thr Thr Leu Ser Ala Ser Ala Leu Ala Val Ala Leu Ala	
125 130 135	

TTC	ATC	ATC	AAG	CCA	GGA	TCC	GGT	GCG	CAG	ACC	CTT	CAG	TCC	AGC	GAC	486
Phe	Ile	Ile	Lys	Pro	Gly	Ser	Gly	Ala	Gln	Thr	Leu	Gln	Ser	Ser	Asp	
			140					145					150			
CTG	GGG	CTG	GAG	GAC	TCG	GGG	CCT	CCT	CCT	GTC	CCC	AAA	GAG	ACG	GTG	534
Leu	Gly	Leu	Glu	Asp	Ser	Gly	Pro	Pro	Pro	Val	Pro	Lys	Glu	Thr	Val	
		155					160					165				
GAC	TCT	TTC	CTC	GAC	CTG	GCC	AGA	AAC	CTG	TTT	CCC	TCC	AAT	CTT	GTG	582
Asp	Ser	Phe	Leu	Asp	Leu	Ala	Arg	Asn	Leu	Phe	Pro	Ser	Asn	Leu	Val	
	170					175					180					
GTT	GCA	GCT	TTC	CGT	ACG	TAT	GCA	ACC	GAT	TAT	AAA	GTC	GTG	ACC	CAG	630
Val	Ala	Ala	Phe	Arg	Thr	Tyr	Ala	Thr	Asp	Tyr	Lys	Val	Val	Thr	Gln	
185				190						195					200	
AAC	AGC	AGC	TCT	GGA	AAT	GTA	ACC	CAT	GAA	AAG	ATC	CCC	ATA	GGC	ACT	678
Asn	Ser	Ser	Ser	Gly	Asn	Val	Thr	His	Glu	Lys	Ile	Pro	Ile	Gly	Thr	
				205					210					215		
GAG	ATA	GAA	GGG	ATG	AAC	ATT	TTA	GGA	TTG	GTC	CTG	TTT	GCT	CTG	GTG	726
Glu	Ile	Glu	Gly	Met	Asn	Ile	Leu	Gly	Leu	Val	Leu	Phe	Ala	Leu	Val	
			220					225					230			
TTA	GGA	GTG	GCC	TTA	AAG	AAA	CTA	GGC	TCC	GAA	GGA	GAA	GAC	CTC	ATC	774
Leu	Gly	Val	Ala	Leu	Lys	Lys	Leu	Gly	Ser	Glu	Gly	Glu	Asp	Leu	Ile	
		235					240					245				
CGT	TTC	TTC	AAT	TCC	CTC	AAC	GAG	GCG	ACG	ATG	GTG	CTG	GTG	TCC	TGG	822
Arg	Phe	Phe	Asn	Ser	Leu	Asn	Glu	Ala	Thr	Met	Val	Leu	Val	Ser	Trp	
	250					255					260					
ATT	ATG	TGG	TAC	GTA	CCT	GTG	GGC	ATC	ATG	TTC	CTT	GTT	GGA	AGC	AAG	870
Ile	Met	Trp	Tyr	Val	Pro	Val	Gly	Ile	Met	Phe	Leu	Val	Gly	Ser	Lys	
265					270					275					280	
ATC	GTG	GAA	ATG	AAA	GAC	ATC	ATC	GTG	CTG	GTG	ACC	AGC	CTG	GGG	AAA	918
Ile	Val	Glu	Met	Lys	Asp	Ile	Ile	Val	Leu	Val	Thr	Ser	Leu	Gly	Lys	
				285					290					295		
TAC	ATC	TTC	GCA	TCT	ATA	TTG	GGC	CAT	GTT	ATT	CAT	GGA	GGA	ATT	GTT	966
Tyr	Ile	Phe	Ala	Ser	Ile	Leu	Gly	His	Val	Ile	His	Gly	Gly	Ile	Val	
			300					305					310			
CTG	CCA	CTT	ATT	TAT	TTT	GTT	TTC	ACA	CGA	AAA	AAC	CCA	TTC	AGA	TTC	1014
Leu	Pro	Leu	Ile	Tyr	Phe	Val	Phe	Thr	Arg	Lys	Asn	Pro	Phe	Arg	Phe	
		315					320					325				
CTC	CTG	GGC	CTC	CTC	GCC	CCA	TTT	GCG	ACA	GCA	TTT	GCT	ACC	TGC	TCC	1062
Leu	Leu	Gly	Leu	Leu	Ala	Pro	Phe	Ala	Thr	Ala	Phe	Ala	Thr	Cys	Ser	
		330				335					340					
AGC	TCA	GCG	ACC	CTT	CCC	TCT	ATG	ATG	AAG	TGC	ATT	GAA	GAG	AAC	AAT	1110
Ser	Ser	Ala	Thr	Leu	Pro	Ser	Met	Met	Lys	Cys	Ile	Glu	Glu	Asn	Asn	
345					350					355					360	
GGT	GTG	GAC	AAG	AGG	ATC	AGC	AGG	TTT	ATT	CTC	CCC	ATC	GGG	GCC	ACC	1158
Gly	Val	Asp	Lys	Arg	Ile	Ser	Arg	Phe	Ile	Leu	Pro	Ile	Gly	Ala	Thr	
				365					370					375		

GTG	AAC	ATG	GAC	GGA	GCA	GCC	ATC	TTC	CAG	TGT	GTG	GCC	GCG	GTG	TTC	1206
Val	Asn	Met	Asp	Gly	Ala	Ala	Ile	Phe	Gln	Cys	Val	Ala	Ala	Val	Phe	
			380					385					390			
ATT	GCG	CAA	CTC	AAC	AAC	ATA	GAG	CTC	AAC	GCA	GGA	CAG	ATT	TTC	ACC	1254
Ile	Ala	Gln	Leu	Asn	Asn	Ile	Glu	Leu	Asn	Ala	Gly	Gln	Ile	Phe	Thr	
		395					400					405				
ATT	CTA	GTG	ACT	GCC	ACA	GCG	TCC	AGT	GTT	GGA	GCA	GCA	GGC	GTG	CCA	1302
Ile	Leu	Val	Thr	Ala	Thr	Ala	Ser	Ser	Val	Gly	Ala	Ala	Gly	Val	Pro	
	410					415					420					
GCT	GGA	GGG	GTC	CTC	ACC	ATT	GCC	ATT	ATC	CTG	GAG	GCC	ATT	GGG	CTG	1350
Ala	Gly	Gly	Val	Leu	Thr	Ile	Ala	Ile	Ile	Leu	Glu	Ala	Ile	Gly	Leu	
425					430					435					440	
CCT	ACT	CAT	GAC	CTG	CCT	CTG	ATC	CTG	GCT	GTG	GAC	TGG	ATT	GTG	GAC	1398
Pro	Thr	His	Asp	Leu	Pro	Leu	Ile	Leu	Ala	Val	Asp	Trp	Ile	Val	Asp	
			445					450						455		
CGG	ACC	ACC	ACG	GTG	GTG	AAT	GTG	GAG	GGG	GAT	GCC	CTG	GGT	GCA	GGC	1446
Arg	Thr	Thr	Thr	Val	Val	Asn	Val	Glu	Gly	Asp	Ala	Leu	Gly	Ala	Gly	
			460					465					470			
ATT	CTC	CAC	CAC	CTG	AAT	CAG	AAG	GCA	ACA	AAG	AAA	GGC	GAG	CAG	GAA	1494
Ile	Leu	His	His	Leu	Asn	Gln	Lys	Ala	Thr	Lys	Lys	Gly	Glu	Gln	Glu	
		475				480						485				
CTT	GCT	GAG	GTG	AAA	GTG	GAA	GCC	ATC	CCC	AAC	TGC	AAG	TCT	GAG	GAG	1542
Leu	Ala	Glu	Val	Lys	Val	Glu	Ala	Ile	Pro	Asn	Cys	Lys	Ser	Glu	Glu	
	490					495					500					
GAG	ACA	TCG	CCC	CTG	GTG	ACA	CAC	CAG	AAC	CCC	GCT	GGC	CCC	GTG	GCC	1590
Glu	Thr	Ser	Pro	Leu	Val	Thr	His	Gln	Asn	Pro	Ala	Gly	Pro	Val	Ala	
505					510					515					520	
AGT	GCC	CCA	GAA	CTG	GAA	TCC	AAG	GAG	TCG	GTT	CTG	TGATGGGGCT				1636
Ser	Ala	Pro	Glu	Leu	Glu	Ser	Lys	Glu	Ser	Val	Leu					
			525					530								
GGGCTTTGGG	CTTGCCTGCC	AGCAGTGATG	TCCCACCCTG	TTCA												1680

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Glu	Lys	Ser	Asn	Glu	Thr	Asn	Gly	Tyr	Leu	Asp	Ser	Ala	Gln	Ala
1				5				10						15	
Gly	Pro	Ala	Ala	Gly	Pro	Gly	Ala	Pro	Gly	Thr	Ala	Ala	Gly	Arg	Ala
		20					25						30		

Arg	Arg	Cys	Ala	Arg	Phe	Leu	Arg	Arg	Gln	Ala	Leu	Val	Leu	Leu	Thr	
		35					40					45				
Val	Ser	Gly	Val	Leu	Ala	Gly	Ala	Gly	Leu	Gly	Ala	Ala	Leu	Arg	Gly	
	50					55					60					
Leu	Ser	Leu	Ser	Arg	Thr	Gln	Val	Thr	Tyr	Leu	Ala	Phe	Pro	Gly	Glu	
65					70					75					80	
Met	Leu	Leu	Arg	Met	Leu	Arg	Met	Ile	Ile	Leu	Pro	Leu	Val	Val	Cys	
				85					90					95		
Ser	Leu	Val	Ser	Gly	Ala	Ala	Ser	Leu	Asp	Ala	Ser	Cys	Leu	Gly	Arg	
			100					105					110			
Leu	Gly	Gly	Ile	Arg	Val	Ala	Tyr	Phe	Gly	Leu	Thr	Thr	Leu	Ser	Ala	
		115					120					125				
Ser	Ala	Leu	Ala	Val	Ala	Leu	Ala	Phe	Ile	Ile	Lys	Pro	Gly	Ser	Gly	
	130					135					140					
Ala	Gln	Thr	Leu	Gln	Ser	Ser	Asp	Leu	Gly	Leu	Glu	Asp	Ser	Gly	Pro	
145					150					155					160	
Pro	Pro	Val	Pro	Lys	Glu	Thr	Val	Asp	Ser	Phe	Leu	Asp	Leu	Ala	Arg	
				165					170					175		
Asn	Leu	Phe	Pro	Ser	Asn	Leu	Val	Val	Ala	Ala	Phe	Arg	Thr	Tyr	Ala	
			180					185					190			
Thr	Asp	Tyr	Lys	Val	Val	Thr	Gln	Asn	Ser	Ser	Ser	Gly	Asn	Val	Thr	
		195					200					205				
His	Glu	Lys	Ile	Pro	Ile	Gly	Thr	Glu	Ile	Glu	Gly	Met	Asn	Ile	Leu	
	210					215					220					
Gly	Leu	Val	Leu	Phe	Ala	Leu	Val	Leu	Gly	Val	Ala	Leu	Lys	Lys	Leu	
225					230					235					240	
Gly	Ser	Glu	Gly	Glu	Asp	Leu	Ile	Arg	Phe	Phe	Asn	Ser	Leu	Asn	Glu	
				245					250					255		
Ala	Thr	Met	Val	Leu	Val	Ser	Trp	Ile	Met	Trp	Tyr	Val	Pro	Val	Gly	
			260					265					270			
Ile	Met	Phe	Leu	Val	Gly	Ser	Lys	Ile	Val	Glu	Met	Lys	Asp	Ile	Ile	
		275					280					285				
Val	Leu	Val	Thr	Ser	Leu	Gly	Lys	Tyr	Ile	Phe	Ala	Ser	Ile	Leu	Gly	
	290					295					300					
His	Val	Ile	His	Gly	Gly	Ile	Val	Leu	Pro	Leu	Ile	Tyr	Phe	Val	Phe	
305					310					315					320	
Thr	Arg	Lys	Asn	Pro	Phe	Arg	Phe	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Phe	
				325					330					335		
Ala	Thr	Ala	Phe	Ala	Thr	Cys	Ser	Ser	Ser	Ala	Thr	Leu	Pro	Ser	Met	
			340					345					350			

Met	Lys	Cys	Ile	Glu	Glu	Asn	Asn	Gly	Val	Asp	Lys	Arg	Ile	Ser	Arg	
		355					360					365				
Phe	Ile	Leu	Pro	Ile	Gly	Ala	Thr	Val	Asn	Met	Asp	Gly	Ala	Ala	Ile	
	370					375					380					
Phe	Gln	Cys	Val	Ala	Ala	Val	Phe	Ile	Ala	Gln	Leu	Asn	Asn	Ile	Glu	
	385				390					395					400	
Leu	Asn	Ala	Gly	Gln	Ile	Phe	Thr	Ile	Leu	Val	Thr	Ala	Thr	Ala	Ser	
				405					410					415		
Ser	Val	Gly	Ala	Ala	Gly	Val	Pro	Ala	Gly	Gly	Val	Leu	Thr	Ile	Ala	
			420					425					430			
Ile	Ile	Leu	Glu	Ala	Ile	Gly	Leu	Pro	Thr	His	Asp	Leu	Pro	Leu	Ile	
		435					440					445				
Leu	Ala	Val	Asp	Trp	Ile	Val	Asp	Arg	Thr	Thr	Thr	Val	Val	Asn	Val	
	450					455					460					
Glu	Gly	Asp	Ala	Leu	Gly	Ala	Gly	Ile	Leu	His	His	Leu	Asn	Gln	Lys	
	465				470					475					480	
Ala	Thr	Lys	Lys	Gly	Glu	Gln	Glu	Leu	Ala	Glu	Val	Lys	Val	Glu	Ala	
				485					490					495		
Ile	Pro	Asn	Cys	Lys	Ser	Glu	Glu	Glu	Thr	Ser	Pro	Leu	Val	Thr	His	
			500					505					510			
Gln	Asn	Pro	Ala	Gly	Pro	Val	Ala	Ser	Ala	Pro	Glu	Leu	Glu	Ser	Lys	
		515					520					525				
Glu	Ser	Val	Leu													
	530															

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..30

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 31..1656

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 1657..1680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAAGAAGAGA CCCTCCTAGA AAAGTAAAAT	ATG ACT AAA AGC AAT GGA GAA GAG	54
	Met Thr Lys Ser Asn Gly Glu Glu	
	1 5	
CCC AAG ATG GGG GGC AGG ATG GAG AGA TTC CAG CAG GGA GTC CGT AAA	102	
Pro Lys Met Gly Gly Arg Met Glu Arg Phe Gln Gln Gly Val Arg Lys		
	10 15 20	
CGC ACA CTT TTG GCC AAG AAG AAA GTG CAG AAC ATT ACA AAG GAG GTT	150	
Arg Thr Leu Leu Ala Lys Lys Lys Val Gln Asn Ile Thr Lys Glu Val		
	25 30 35 40	
GTT AAA AGT TAC CTG TTT CGG AAT GCT TTT GTG CTG CTC ACA GTC ACC	198	
Val Lys Ser Tyr Leu Phe Arg Asn Ala Phe Val Leu Leu Thr Val Thr		
	45 50 55	
GCT GTC ATT GTG GGT ACA ATC CTT GGA TTT ACC CTC CGA CCA TAC AGA	246	
Ala Val Ile Val Gly Thr Ile Leu Gly Phe Thr Leu Arg Pro Tyr Arg		
	60 65 70	
ATG AGC TAC CGG GAA GTC AAG TAC TTC TCC TTT CCT GGG GAA CTT CTG	294	
Met Ser Tyr Arg Glu Val Lys Tyr Phe Ser Phe Pro Gly Glu Leu Leu		
	75 80 85	
ATG AGG ATG TTA CAG ATG CTG GTC TTA CCA CTT ATC ATC TCC AGT CTT	342	
Met Arg Met Leu Gln Met Leu Val Leu Pro Leu Ile Ile Ser Ser Leu		
	90 95 100	
GTC ACA GGA ATG GCG GCG CTA GAT AGT AAG GCA TCA GGG AAG TGG GAA	390	
Val Thr Gly Met Ala Ala Leu Asp Ser Lys Ala Ser Gly Lys Trp Glu		
	105 110 115 120	
TGC GGA GCT GTA GTC TAT TAT ATG ACT ACC ACC ATC ATT GCT GTG GTG	438	
Cys Gly Ala Val Val Tyr Tyr Met Thr Thr Thr Ile Ile Ala Val Val		
	125 130 135	
ATT GGC ATA ATC ATT GTC ATC ATC ATC CAT CCT GGG AAG GGC ACA AAG	486	
Ile Gly Ile Ile Ile Val Ile Ile Ile Ile His Pro Gly Lys Gly Thr Lys		
	140 145 150	
GAA AAC ATG CAC AGA GAA GGC AAA ATT GTA CGA GTG ACA GCT GCA GAT	534	
Glu Asn Met His Arg Glu Gly Lys Ile Val Arg Val Thr Ala Ala Asp		
	155 160 165	
GCC TTC CTG GAC TTG ATC AGG AAC ATG TTA AAT CCA AAT CTG GTA GAA	582	
Ala Phe Leu Asp Leu Ile Arg Asn Met Leu Asn Pro Asn Leu Val Glu		
	170 175 180	
GCC TGC TTT AAA CAG TTT AAA ACC AAC TAT GAG AAG AGA AGC TTT AAA	630	
Ala Cys Phe Lys Gln Phe Lys Thr Asn Tyr Glu Lys Arg Ser Phe Lys		
	185 190 195 200	
GTG CCC ATC CAG GCC AAC GAA ACG CTT GTG GGT GCT GTG ATA AAC AAT	678	
Val Pro Ile Gln Ala Asn Glu Thr Leu Val Gly Ala Val Ile Asn Asn		
	205 210 215	
GTG TCT GAG GCC ATG GAG ACT CTT ACC CGA ATC ACA GAG GAG CTG GTC	726	
Val Ser Glu Ala Met Glu Thr Leu Thr Arg Ile Thr Glu Glu Leu Val		
	220 225 230	



CCA Pro	GTT Val	CCA Pro 235	GGA Gly	TCT Ser	GTG Val	AAT Asn	GGA Gly 240	GTC Val	AAT Asn	GCC Ala	CTG Leu 245	GGT Gly	CTA Leu	GTT Val	GTC Val	774
TTC Phe	TCC Ser 250	ATG Met	TGC Cys	TTC Phe	GGT Gly	TTT Phe 255	GTG Val	ATT Ile	GGA Gly	AAC Asn 260	ATG Met	AAG Lys	GAA Glu	CAG Gln	GGG Gly	822
CAG Gln 265	GCC Ala	CTG Leu	AGA Arg	GAG Glu	TTC Phe 270	TTT Phe	GAT Asp	TCT Ser	CTT Leu	AAC Asn 275	GAA Glu	GCC Ala	ATC Ile	ATG Met	AGA Arg 280	870
CTG Leu	GTA Val	GCA Ala	GTA Val 285	ATA Ile	ATG Met	TGG Trp	TAT Tyr	GCC Ala	CCC Pro 290	GTG Val	GGT Gly	ATT Ile	CTC Leu	TTC Phe 295	CTG Leu	918
ATT Ile	GCT Ala	GGG Gly	AAG Lys 300	ATT Ile	GTG Val	GAG Glu	ATG Met 305	GAA Glu	GAC Asp	ATG Met	GGT Gly	GTG Val	ATT Ile 310	GGG Gly	GGG Gly	966
CAG Gln	CTT Leu 315	GCC Ala	ATG Met	TAC Tyr	ACC Thr	GTG Val	ACT Thr 320	GTC Val	ATT Ile	GTT Val	GGC Gly 325	TTA Leu	CTC Leu	ATT Ile	CAC His	1014
GCA Ala 330	GTC Val	ATC Ile	GTC Val	TTG Leu	CCA Pro 335	CTC Leu	CTC Leu	TAC Tyr	TTC Phe	TTG Leu 340	GTA Val	ACA Thr	CGG Arg	AAA Lys	AAC Asn	1062
CCT Pro 345	TGG Trp	GTT Val	TTT Phe	ATT Ile	GGA Gly 350	GGG Gly	TTG Leu	CTG Leu	CAA Gln 355	GCA Ala	CTC Leu	ATC Ile	ACC Thr	GCT Ala	CTG Leu 360	1110
GGG Gly	ACC Thr	TCT Ser	TCA Ser 365	AGT Ser	TCT Ser	GCC Ala	ACC Thr	CTA Leu	CCC Pro 370	ATC Ile	ACC Thr	TTC Phe	AAG Lys	TGC Cys 375	CTG Leu	1158
GAA Glu	GAG Glu	AAC Asn 380	AAT Asn	GGC Gly	GTG Val	GAC Asp	AAG Lys 385	CGC Arg	GTC Val	ACC Thr	AGA Arg	TTC Phe 390	GTG Val	CTC Leu	CCC Pro	1206
GTA Val	GGA Gly 395	GCC Ala	ACC Thr	ATT Ile	AAC Asn	ATG Met	GAT Asp 400	GGG Gly	ACT Thr	GCC Ala	CTC Leu	TAT Tyr 405	GAG Glu	GCT Ala	TTG Leu	1254
GCT Ala 410	GCC Ala	ATT Ile	TTC Phe	ATT Ile	GCT Ala 415	CAA Gln	GTT Val	AAC Asn	AAC Asn	TTT Phe	GAA Glu 420	CTG Leu	AAC Asn	TTC Phe	GGA Gly	1302
CAA Gln 425	ATT Ile	ATT Ile	ACA Thr	ATC Ile	AGC Ser 430	ATC Ile	ACA Thr	GCC Ala	ACA Thr	GCT Ala 435	GCC Ala	AGT Ser	ATT Ile	GGG Gly	GCA Ala 440	1350
GCT Ala	GGA Gly	ATT Ile	CCT Pro	CAG Gln 445	GCG Ala	GGC Gly	CTG Leu	GTC Val	ACT Thr 450	ATG Met	GTC Val	ATT Ile	GTG Val	CTG Leu 455	ACA Thr	1398
TCT Ser	GTC Val	GGC Gly	CTG Leu 460	CCC Pro	ACT Thr	GAC Asp	GAC Asp	ATC Ile 465	ACG Thr	CTC Leu	ATC Ile	ATC Ile	GCG Ala 470	GTG Val	GAC Asp	1446

TGG	TTC	TTG	GAT	CGC	CTC	CGG	ACC	ACC	ACC	AAC	GTA	CTG	GGA	GAC	TCC	1494
Trp	Phe	Leu	Asp	Arg	Leu	Arg	Thr	Thr	Thr	Asn	Val	Leu	Gly	Asp	Ser	
		475					480					485				
CTG	GGA	GCT	GGG	ATT	GTG	GAG	CAC	TTG	TCA	CGA	CAT	GAA	CTG	AAG	AAC	1542
Leu	Gly	Ala	Gly	Ile	Val	Glu	His	Leu	Ser	Arg	His	Glu	Leu	Lys	Asn	
	490					495					500					
AGA	GAT	GTT	GAA	ATG	GGT	AAC	TCA	GTG	ATT	GAA	GAG	AAT	GAA	ATG	AAG	1590
Arg	Asp	Val	Glu	Met	Gly	Asn	Ser	Val	Ile	Glu	Glu	Asn	Glu	Met	Lys	
505					510					515					520	
AAA	CCA	TAT	CAA	CTG	ATT	GCA	CAG	GAC	AAT	GAA	ACT	GAG	AAA	CCC	ATC	1638
Lys	Pro	Tyr	Gln	Leu	Ile	Ala	Gln	Asp	Asn	Glu	Thr	Glu	Lys	Pro	Ile	
				525					530					535		
GAC	AGT	GAA	ACC	AAG	ATG	TAGACTAACA TAAAGAAACA CTTT										1680
Asp	Ser	Glu	Thr	Lys	Met											
			540													

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Thr	Lys	Ser	Asn	Gly	Glu	Glu	Pro	Lys	Met	Gly	Gly	Arg	Met	Glu
1				5					10					15	
Arg	Phe	Gln	Gln	Gly	Val	Arg	Lys	Arg	Thr	Leu	Leu	Ala	Lys	Lys	Lys
			20					25					30		
Val	Gln	Asn	Ile	Thr	Lys	Glu	Val	Val	Lys	Ser	Tyr	Leu	Phe	Arg	Asn
		35					40					45			
Ala	Phe	Val	Leu	Leu	Thr	Val	Thr	Ala	Val	Ile	Val	Gly	Thr	Ile	Leu
		50				55					60				
Gly	Phe	Thr	Leu	Arg	Pro	Tyr	Arg	Met	Ser	Tyr	Arg	Glu	Val	Lys	Tyr
65					70					75				80	
Phe	Ser	Phe	Pro	Gly	Glu	Leu	Leu	Met	Arg	Met	Leu	Gln	Met	Leu	Val
				85					90					95	
Leu	Pro	Leu	Ile	Ile	Ser	Ser	Leu	Val	Thr	Gly	Met	Ala	Ala	Leu	Asp
			100					105					110		
Ser	Lys	Ala	Ser	Gly	Lys	Trp	Glu	Cys	Gly	Ala	Val	Val	Tyr	Tyr	Met
		115					120					125			
Thr	Thr	Thr	Ile	Ile	Ala	Val	Val	Ile	Gly	Ile	Ile	Ile	Val	Ile	Ile
						130		135			140				

Ile	His	Pro	Gly	Lys	Gly	Thr	Lys	Glu	Asn	Met	His	Arg	Glu	Gly	Lys	145	150	155	160
Ile	Val	Arg	Val	Thr	Ala	Ala	Asp	Ala	Phe	Leu	Asp	Leu	Ile	Arg	Asn	165	170	175	
Met	Leu	Asn	Pro	Asn	Leu	Val	Glu	Ala	Cys	Phe	Lys	Gln	Phe	Lys	Thr	180	185	190	
Asn	Tyr	Glu	Lys	Arg	Ser	Phe	Lys	Val	Pro	Ile	Gln	Ala	Asn	Glu	Thr	195	200	205	
Leu	Val	Gly	Ala	Val	Ile	Asn	Asn	Val	Ser	Glu	Ala	Met	Glu	Thr	Leu	210	215	220	
Thr	Arg	Ile	Thr	Glu	Glu	Leu	Val	Pro	Val	Pro	Gly	Ser	Val	Asn	Gly	225	230	235	240
Val	Asn	Ala	Leu	Gly	Leu	Val	Val	Phe	Ser	Met	Cys	Phe	Gly	Phe	Val	245	250	255	
Ile	Gly	Asn	Met	Lys	Glu	Gln	Gly	Gln	Ala	Leu	Arg	Glu	Phe	Phe	Asp	260	265	270	
Ser	Leu	Asn	Glu	Ala	Ile	Met	Arg	Leu	Val	Ala	Val	Ile	Met	Trp	Tyr	275	280	285	
Ala	Pro	Val	Gly	Ile	Leu	Phe	Leu	Ile	Ala	Gly	Lys	Ile	Val	Glu	Met	290	295	300	
Glu	Asp	Met	Gly	Val	Ile	Gly	Gly	Gln	Leu	Ala	Met	Tyr	Thr	Val	Thr	305	310	315	320
Val	Ile	Val	Gly	Leu	Leu	Ile	His	Ala	Val	Ile	Val	Leu	Pro	Leu	Leu	325	330	335	
Tyr	Phe	Leu	Val	Thr	Arg	Lys	Asn	Pro	Trp	Val	Phe	Ile	Gly	Gly	Leu	340	345	350	
Leu	Gln	Ala	Leu	Ile	Thr	Ala	Leu	Gly	Thr	Ser	Ser	Ser	Ser	Ala	Thr	355	360	365	
Leu	Pro	Ile	Thr	Phe	Lys	Cys	Leu	Glu	Glu	Asn	Asn	Gly	Val	Asp	Lys	370	375	380	
Arg	Val	Thr	Arg	Phe	Val	Leu	Pro	Val	Gly	Ala	Thr	Ile	Asn	Met	Asp	385	390	395	400
Gly	Thr	Ala	Leu	Tyr	Glu	Ala	Leu	Ala	Ala	Ile	Phe	Ile	Ala	Gln	Val	405	410	415	
Asn	Asn	Phe	Glu	Leu	Asn	Phe	Gly	Gln	Ile	Ile	Thr	Ile	Ser	Ile	Thr	420	425	430	
Ala	Thr	Ala	Ala	Ser	Ile	Gly	Ala	Ala	Gly	Ile	Pro	Gln	Ala	Gly	Leu	435	440	445	
Val	Thr	Met	Val	Ile	Val	Leu	Thr	Ser	Val	Gly	Leu	Pro	Thr	Asp	Asp	450	455	460	

Ile	Thr	Leu	Ile	Ile	Ala	Val	Asp	Trp	Phe	Leu	Asp	Arg	Leu	Arg	Thr	
465					470					475					480	
Thr	Thr	Asn	Val	Leu	Gly	Asp	Ser	Leu	Gly	Ala	Gly	Ile	Val	Glu	His	
				485					490					495		
Leu	Ser	Arg	His	Glu	Leu	Lys	Asn	Arg	Asp	Val	Glu	Met	Gly	Asn	Ser	
			500					505					510			
Val	Ile	Glu	Glu	Asn	Glu	Met	Lys	Lys	Pro	Tyr	Gln	Leu	Ile	Ala	Gln	
		515					520					525				
Asp	Asn	Glu	Thr	Glu	Lys	Pro	Ile	Asp	Ser	Glu	Thr	Lys	Met			
530						535					540					

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..33

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 34..1755

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 1756..1800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATAGTGCTG AAGAGGAGGG GCGTTCCCAG ACC ATG GCA TCT ACG GAA GGT GCC	54
Met Ala Ser Thr Glu Gly Ala	
1 5	
AAC AAT ATG CCC AAG CAG GTG GAA GTG CGA ATG CCA GAC AGT CAT CTT	102
Asn Asn Met Pro Lys Gln Val Glu Val Arg Met Pro Asp Ser His Leu	
10 15 20	
GGC TCA GAG GAA CCC AAG CAC CGG CAC CTG GGC CTG CGC CTG TGT GAC	150
Gly Ser Glu Glu Pro Lys His Arg His Leu Gly Leu Arg Leu Cys Asp	
25 30 35	
AAG CTG GGG AAG AAT CTG CTG CTC ACC CTG ACG GTG TTT GGT GTC ATC	198
Lys Leu Gly Lys Asn Leu Leu Leu Thr Leu Thr Val Phe Gly Val Ile	
40 45 50 55	
CTG GGA GCA GTG TGT GGA GGG CTT CTT CGC TTG GCA TCT CCC ATC CAC	246
Leu Gly Ala Val Cys Gly Gly Leu Leu Arg Leu Ala Ser Pro Ile His	
60 65 70	

CCT Pro	GAT Asp	GTG Val	GTT Val 75	ATG Met	TTA Leu	ATA Ile	GCC Ala	TTC Phe 80	CCA Pro	GGG Gly	GAT Asp	ATA Ile	CTC Leu 85	ATG Met	AGG Arg	294
ATG Met	CTA Leu	AAA Lys 90	ATG Met	CTC Leu	ATT Ile	CTG Leu	GGT Gly 95	CTA Leu	ATC Ile	ATC Ile	TCC Ser	AGC Ser 100	TTA Leu	ATC Ile	ACA Thr	342
GGG Gly	TTG Leu 105	TCA Ser	GGC Gly	CTG Leu	GAT Asp	GCT Ala 110	AAG Lys	GCT Ala	AGT Ser	GGC Gly	CGC Arg 115	TTG Leu	GGC Gly	ACG Thr	AGA Arg	390
GCC Ala 120	ATG Met	GTG Val	TAT Tyr	TAC Tyr	ATG Met 125	TCC Ser	ACG Thr	ACC Thr	ATC Ile	ATT Ile 130	GCT Ala	GCA Ala	GTA Val	CTG Leu	GGG Gly 135	438
GTC Val	ATT Ile	CTG Leu	GTC Val	TTG Leu 140	GCT Ala	ATC Ile	CAT His	CCA Pro	GGC Gly 145	AAT Asn	CCC Pro	AAG Lys	CTC Leu	AAG Lys 150	AAG Lys	486
CAG Gln	CTG Leu	GGG Gly 155	CCT Pro	GGG Gly	AAG Lys	AAG Lys	AAT Asn	GAT Asp 160	GAA Glu	GTG Val	TCC Ser	AGC Ser	CTG Leu 165	GAT Asp	GCC Ala	534
TTC Phe	CTG Leu 170	GAC Asp	CTT Leu	ATT Ile	CGA Arg	AAT Asn	CTC Leu 175	TTC Phe	CCT Pro	GAA Glu	AAC Asn	CTT Leu 180	GTC Val	CAA Gln	GCC Ala	582
TGC Cys	TTT Phe 185	CAA Gln	CAG Gln	ATT Ile	CAA Gln	ACA Thr 190	GTG Val	ACG Thr	AAG Lys	AAA Lys	GTC Val 195	CTG Leu	GTT Val	GCA Ala	CCA Pro	630
CCG Pro 200	CCA Pro	GAC Asp	GAG Glu	GAG Glu	GCC Ala 205	AAC Asn	GCA Ala	ACC Thr	AGC Ser	GCT Ala 210	GAA Glu	GTC Val	TCT Ser	CTG Leu	TTG Leu 215	678
AAC Asn	GAG Glu	ACT Thr	GTG Val	ACT Thr 220	GAG Glu	GTG Val	CCG Pro	GAG Glu 225	GAG Glu	ACT Thr	AAG Lys	ATG Met	GTT Val 230	ATC Ile	AAG Lys	726
AAG Lys	GGC Gly	CTG Leu	GAG Glu 235	TTC Phe	AAG Lys	GAT Asp	GGG Gly 240	ATG Met	AAC Asn	GTC Val	TTA Leu	GGT Gly 245	CTG Leu 245	ATA Ile	GGG Gly	774
TTT Phe	TTC Phe	ATT Ile 250	GCT Ala	TTT Phe	GGC Gly	ATC Ile	GCT Ala 255	ATG Met	GGG Gly	AAG Lys	ATG Met	GGA Gly 260	GAT Asp	CAG Gln	GCC Ala	822
AAG Lys 265	CTG Leu	ATG Met	GTG Val	GAT Asp	TTC Phe	TTC Phe 270	AAC Asn	ATT Ile	TTG Leu	AAT Asn	GAG Glu 275	ATT Ile	GTA Val	ATG Met	AAG Lys	870
TTA Leu 280	GTG Val	ATC Ile	ATG Met	ATC Ile	ATG Met 285	TGG Trp	TAC Tyr	TCT Ser	CCC Pro	CTG Leu 290	GGT Gly	ATC Ile	GCC Ala	TGC Cys	CTG Leu 295	918
ATC Ile	TGT Cys	GGA Gly	AAG Lys	ATC Ile 300	ATT Ile	GCA Ala	ATC Ile	AAG Lys	GAC Asp 305	TTA Leu	GAA Glu	GTG Val	GTT Val	GCT Ala 310	AGG Arg	966

CAA	CTG	GGG	ATG	TAC	ATG	GTA	ACA	GTG	ATC	ATA	GGC	CTC	ATC	ATC	CAC	1014
Gln	Leu	Gly	Met	Tyr	Met	Val	Thr	Val	Ile	Ile	Gly	Leu	Ile	Ile	His	
			315					320					325			
GGG	GGC	ATC	TTT	CTC	CCC	TTG	ATT	TAC	TTT	GTA	GTG	ACC	AGG	AAA	AAC	1062
Gly	Gly	Ile	Phe	Leu	Pro	Leu	Ile	Tyr	Phe	Val	Val	Thr	Arg	Lys	Asn	
		330					335					340				
CCC	TTC	TCC	CTT	TTT	GCT	GGC	ATT	TTC	CAA	GCT	TGG	ATC	ACT	GCC	CTG	1110
Pro	Phe	Ser	Leu	Phe	Ala	Gly	Ile	Phe	Gln	Ala	Trp	Ile	Thr	Ala	Leu	
	345					350					355					
GGC	ACC	GCT	TCC	AGT	GCT	GGA	ACT	TTG	CCT	GTC	ACC	TTT	CGT	TGC	CTG	1158
Gly	Thr	Ala	Ser	Ser	Ala	Gly	Thr	Leu	Pro	Val	Thr	Phe	Arg	Cys	Leu	
360					365					370					375	
GAA	GAA	AAT	CTG	GGG	ATT	GAT	AAG	CGT	GTG	ACT	AGA	TTC	GTC	CTT	CCT	1206
Glu	Glu	Asn	Leu	Gly	Ile	Asp	Lys	Arg	Val	Thr	Arg	Phe	Val	Leu	Pro	
			380					385						390		
GTT	GGA	GCA	ACC	ATT	AAC	ATG	GAT	GGT	ACA	GCC	CTT	TAT	GAA	GCG	GTG	1254
Val	Gly	Ala	Thr	Ile	Asn	Met	Asp	Gly	Thr	Ala	Leu	Tyr	Glu	Ala	Val	
			395					400					405			
GCC	GCC	ATC	TTT	ATA	GCC	CAA	ATG	AAT	GGT	GTT	GTC	CTG	GAT	GGA	GGA	1302
Ala	Ala	Ile	Phe	Ile	Ala	Gln	Met	Asn	Gly	Val	Val	Leu	Asp	Gly	Gly	
		410					415					420				
CAG	ATT	GTG	ACT	GTA	AGC	CTC	ACA	GCC	ACC	CTG	GCA	AGC	GTC	GGC	GCG	1350
Gln	Ile	Val	Thr	Val	Ser	Leu	Thr	Ala	Thr	Leu	Ala	Ser	Val	Gly	Ala	
	425					430					435					
GCC	AGT	ATC	CCC	AGT	GCC	GGG	CTG	GTC	ACC	ATG	CTC	CTC	ATT	CTG	ACA	1398
Ala	Ser	Ile	Pro	Ser	Ala	Gly	Leu	Val	Thr	Met	Leu	Leu	Ile	Leu	Thr	
440					445					450					455	
GCC	GTG	GGC	CTG	CCA	ACA	GAG	GAC	ATC	AGC	TTG	CTG	GTG	GCT	GTG	GAC	1446
Ala	Val	Gly	Leu	Pro	Thr	Glu	Asp	Ile	Ser	Leu	Leu	Val	Ala	Val	Asp	
			460					465						470		
TGG	CTG	CTG	GAC	AGG	ATG	AGA	ACT	TCA	GTC	AAT	GTT	GTG	GGT	GAC	TCT	1494
Trp	Leu	Leu	Asp	Arg	Met	Arg	Thr	Ser	Val	Asn	Val	Val	Gly	Asp	Ser	
			475					480					485			
TTT	GGG	GCT	GGG	ATA	GTC	TAT	CAC	CTC	TCC	AAG	TCT	GAG	CTG	GAT	ACC	1542
Phe	Gly	Ala	Gly	Ile	Val	Tyr	His	Leu	Ser	Lys	Ser	Glu	Leu	Asp	Thr	
		490					495					500				
ATT	GAC	TCC	CAG	CAT	CGA	GTG	CAT	GAA	GAT	ATT	GAA	ATG	ACC	AAG	ACT	1590
Ile	Asp	Ser	Gln	His	Arg	Val	His	Glu	Asp	Ile	Glu	Met	Thr	Lys	Thr	
	505					510					515					
CAA	TCC	ATT	TAT	GAT	GAC	ATG	AAG	AAC	CAC	AGG	GAA	AGC	AAC	TCT	AAT	1638
Gln	Ser	Ile	Tyr	Asp	Asp	Met	Lys	Asn	His	Arg	Glu	Ser	Asn	Ser	Asn	
520					525					530					535	
CAA	TGT	GTC	TAT	GCT	GCA	CAC	AAC	TCT	GTC	ATA	GTA	GAT	GAA	TGC	AAG	1686
Gln	Cys	Val	Tyr	Ala	Ala	His	Asn	Ser	Val	Ile	Val	Asp	Glu	Cys	Lys	
				540					545					550		

GTA	ACT	CTG	GCA	GCC	AAT	GGA	AAG	TCA	GCC	GAC	TGC	AGT	GTT	GAG	GAA	1734
Val	Thr	Leu	Ala	Ala	Asn	Gly	Lys	Ser	Ala	Asp	Cys	Ser	Val	Glu	Glu	
			555					560					565			

GAA	CCT	TGG	AAA	CGT	GAG	AAA	TAAGGATATG	AGTCTCAGCA	AATTCTTGAA	1785
Glu	Pro	Trp	Lys	Arg	Glu	Lys				
			570							

TAAACTCCCC	AGCGT	1800
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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ala	Ser	Thr	Glu	Gly	Ala	Asn	Asn	Met	Pro	Lys	Gln	Val	Glu	Val	
1				5					10					15		
Arg	Met	Pro	Asp	Ser	His	Leu	Gly	Ser	Glu	Glu	Pro	Lys	His	Arg	His	
			20					25					30			
Leu	Gly	Leu	Arg	Leu	Cys	Asp	Lys	Leu	Gly	Lys	Asn	Leu	Leu	Leu	Thr	
		35					40					45				
Leu	Thr	Val	Phe	Gly	Val	Ile	Leu	Gly	Ala	Val	Cys	Gly	Gly	Leu	Leu	
	50					55					60					
Arg	Leu	Ala	Ser	Pro	Ile	His	Pro	Asp	Val	Val	Met	Leu	Ile	Ala	Phe	
	65				70				75					80		
Pro	Gly	Asp	Ile	Leu	Met	Arg	Met	Leu	Lys	Met	Leu	Ile	Leu	Gly	Leu	
				85					90					95		
Ile	Ile	Ser	Ser	Leu	Ile	Thr	Gly	Leu	Ser	Gly	Leu	Asp	Ala	Lys	Ala	
			100					105					110			
Ser	Gly	Arg	Leu	Gly	Thr	Arg	Ala	Met	Val	Tyr	Tyr	Met	Ser	Thr	Thr	
		115					120					125				
Ile	Ile	Ala	Ala	Val	Leu	Gly	Val	Ile	Leu	Val	Leu	Ala	Ile	His	Pro	
	130					135					140					
Gly	Asn	Pro	Lys	Leu	Lys	Lys	Gln	Leu	Gly	Pro	Gly	Lys	Lys	Asn	Asp	
	145				150					155				160		
Glu	Val	Ser	Ser	Leu	Asp	Ala	Phe	Leu	Asp	Leu	Ile	Arg	Asn	Leu	Phe	
				165					170					175		
Pro	Glu	Asn	Leu	Val	Gln	Ala	Cys	Phe	Gln	Gln	Ile	Gln	Thr	Val	Thr	
			180				185						190			
Lys	Lys	Val	Leu	Val	Ala	Pro	Pro	Pro	Asp	Glu	Glu	Ala	Asn	Ala	Thr	

195				200				205							
Ser	Ala	Glu	Val	Ser	Leu	Leu	Asn	Glu	Thr	Val	Thr	Glu	Val	Pro	Glu
	210					215					220				
Glu	Thr	Lys	Met	Val	Ile	Lys	Lys	Gly	Leu	Glu	Phe	Lys	Asp	Gly	Met
225					230					235					240
Asn	Val	Leu	Gly	Leu	Ile	Gly	Phe	Phe	Ile	Ala	Phe	Gly	Ile	Ala	Met
				245					250					255	
Gly	Lys	Met	Gly	Asp	Gln	Ala	Lys	Leu	Met	Val	Asp	Phe	Phe	Asn	Ile
			260					265						270	
Leu	Asn	Glu	Ile	Val	Met	Lys	Leu	Val	Ile	Met	Ile	Met	Trp	Tyr	Ser
		275					280					285			
Pro	Leu	Gly	Ile	Ala	Cys	Leu	Ile	Cys	Gly	Lys	Ile	Ile	Ala	Ile	Lys
	290					295					300				
Asp	Leu	Glu	Val	Val	Ala	Arg	Gln	Leu	Gly	Met	Tyr	Met	Val	Thr	Val
305					310					315					320
Ile	Ile	Gly	Leu	Ile	Ile	His	Gly	Gly	Ile	Phe	Leu	Pro	Leu	Ile	Tyr
				325					330					335	
Phe	Val	Val	Thr	Arg	Lys	Asn	Pro	Phe	Ser	Leu	Phe	Ala	Gly	Ile	Phe
			340					345					350		
Gln	Ala	Trp	Ile	Thr	Ala	Leu	Gly	Thr	Ala	Ser	Ser	Ala	Gly	Thr	Leu
		355					360					365			
Pro	Val	Thr	Phe	Arg	Cys	Leu	Glu	Glu	Asn	Leu	Gly	Ile	Asp	Lys	Arg
						375					380				
Val	Thr	Arg	Phe	Val	Leu	Pro	Val	Gly	Ala	Thr	Ile	Asn	Met	Asp	Gly
385					390					395					400
Thr	Ala	Leu	Tyr	Glu	Ala	Val	Ala	Ala	Ile	Phe	Ile	Ala	Gln	Met	Asn
				405					410					415	
Gly	Val	Val	Leu	Asp	Gly	Gly	Gln	Ile	Val	Thr	Val	Ser	Leu	Thr	Ala
			420					425					430		
Thr	Leu	Ala	Ser	Val	Gly	Ala	Ala	Ser	Ile	Pro	Ser	Ala	Gly	Leu	Val
		435					440					445			
Thr	Met	Leu	Leu	Ile	Leu	Thr	Ala	Val	Gly	Leu	Pro	Thr	Glu	Asp	Ile
	450					455					460				
Ser	Leu	Leu	Val	Ala	Val	Asp	Trp	Leu	Leu	Asp	Arg	Met	Arg	Thr	Ser
465					470					475				480	
Val	Asn	Val	Val	Gly	Asp	Ser	Phe	Gly	Ala	Gly	Ile	Val	Tyr	His	Leu
				485					490					495	
Ser	Lys	Ser	Glu	Leu	Asp	Thr	Ile	Asp	Ser	Gln	His	Arg	Val	His	Glu
			500					505					510		



Asp	Ile	Glu	Met	Thr	Lys	Thr	Gln	Ser	Ile	Tyr	Asp	Asp	Met	Lys	Asn
		515					520					525			
His	Arg	Glu	Ser	Asn	Ser	Asn	Gln	Cys	Val	Tyr	Ala	Ala	His	Asn	Ser
	530					535					540				
Val	Ile	Val	Asp	Glu	Cys	Lys	Val	Thr	Leu	Ala	Ala	Asn	Gly	Lys	Ser
	545				550					555					560
Ala	Asp	Cys	Ser	Val	Glu	Glu	Glu	Pro	Trp	Lys	Arg	Glu	Lys		
				565					570						

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..15

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 16..1590

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 1591..1674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATAGCGGCGA CAGCC ATG GGG AAA CCG GCG AGG AAA GGA TGC CCG AGT TGG	51
Met Gly Lys Pro Ala Arg Lys Gly Cys Pro Ser Trp	
1 5 10	
AAG CGC TTC CTG AAG AAT AAC TGG GTG TTG CTG TCC ACC GTG GCC GCG	99
Lys Arg Phe Leu Lys Asn Asn Trp Val Leu Leu Ser Thr Val Ala Ala	
15 20 25	
GTG GTG CTA GGC ATT ACC ACA GGA GTC TTG GTT CGA GAA CAC AGC AAC	147
Val Val Leu Gly Ile Thr Thr Gly Val Leu Val Arg Glu His Ser Asn	
30 35 40	
CTC TCA ACT CTA GAG AAA TTC TAC TTT GCT TTT CCT GGA GAA ATT CTA	195
Leu Ser Thr Leu Glu Lys Phe Tyr Phe Ala Phe Pro Gly Glu Ile Leu	
45 50 55 60	
ATG CGG ATG CTG AAA CTC ATC ATT TTG CCA TTA ATT ATA TCC AGC ATG	243
Met Arg Met Leu Lys Leu Ile Ile Leu Pro Leu Ile Ile Ser Ser Met	
65 70 75	
ATT ACA GGT GTT GCT GCA CTG GAT TCC AAC GTA TCC GGA AAA ATT GGT	291
Ile Thr Gly Val Ala Ala Leu Asp Ser Asn Val Ser Gly Lys Ile Gly	
80 85 90	

CTG	CGC	GCT	GTC	GTG	TAT	TAT	TTC	TGT	ACC	ACT	CTC	ATT	GCT	GTT	ATT	339
Leu	Arg	Ala	Val	Val	Tyr	Tyr	Phe	Cys	Thr	Thr	Leu	Ile	Ala	Val	Ile	
		95					100					105				
CTA	GGT	ATT	GTG	CTG	GTG	GTG	AGC	ATC	AAG	CCT	GGT	GTC	ACC	CAG	AAA	387
Leu	Gly	Ile	Val	Leu	Val	Val	Ser	Ile	Lys	Pro	Gly	Val	Thr	Gln	Lys	
	110					115					120					
GTG	GGT	GAA	ATT	GCG	AGG	ACA	GGC	AGC	ACC	CCT	GAA	GTC	AGT	ACG	GTG	435
Val	Gly	Glu	Ile	Ala	Arg	Thr	Gly	Ser	Thr	Pro	Glu	Val	Ser	Thr	Val	
125					130					135					140	
GAT	GCC	ATG	TTA	GAT	CTC	ATC	AGG	AAT	ATG	TTC	CCT	GAG	AAT	CTT	GTC	483
Asp	Ala	Met	Leu	Asp	Leu	Ile	Arg	Asn	Met	Phe	Pro	Glu	Asn	Leu	Val	
				145					150					155		
CAG	GCC	TGT	TTT	CAG	CAG	TAC	AAA	ACT	AAG	CGT	GAA	GAA	GTG	AAG	CCT	531
Gln	Ala	Cys	Phe	Gln	Gln	Tyr	Lys	Thr	Lys	Arg	Glu	Glu	Val	Lys	Pro	
			160					165					170			
CCC	AGC	GAT	CCA	GAG	ATG	AAC	ATG	ACA	GAA	GAG	TCC	TTC	ACA	GCT	GTC	579
Pro	Ser	Asp	Pro	Glu	Met	Asn	Met	Thr	Glu	Glu	Ser	Phe	Thr	Ala	Val	
		175					180						185			
ATG	ACA	ACT	GCA	ATT	TCC	AAG	AAC	AAA	ACA	AAG	GAA	TAC	AAA	ATT	GTT	627
Met	Thr	Thr	Ala	Ile	Ser	Lys	Asn	Lys	Thr	Lys	Glu	Tyr	Lys	Ile	Val	
	190					195					200					
GGC	ATG	TAT	TCA	GAT	GGC	ATA	AAC	GTC	CTG	GGC	TTG	ATT	GTC	TTT	TGC	675
Gly	Met	Tyr	Ser	Asp	Gly	Ile	Asn	Val	Leu	Gly	Leu	Ile	Val	Phe	Cys	
205					210					215					220	
CTT	GTC	TTT	GGA	CTT	GTC	ATT	GGA	AAA	ATG	GGA	GAA	AAG	GGA	CAA	ATT	723
Leu	Val	Phe	Gly	Leu	Val	Ile	Gly	Lys	Met	Gly	Glu	Lys	Gly	Gln	Ile	
				225					230					235		
CTG	GTG	GAT	TTC	TTC	AAT	GCT	TTG	AGT	GAT	GCA	ACC	ATG	AAA	ATC	GTT	771
Leu	Val	Asp	Phe	Phe	Asn	Ala	Leu	Ser	Asp	Ala	Thr	Met	Lys	Ile	Val	
			240					245					250			
CAG	ATC	ATC	ATG	TGT	TAT	ATG	CCA	CTA	GGT	ATT	TTG	TTC	CTG	ATT	GCT	819
Gln	Ile	Ile	Met	Cys	Tyr	Met	Pro	Leu	Gly	Ile	Leu	Phe	Leu	Ile	Ala	
		255					260					265				
GGG	AAG	ATC	ATA	GAA	GTT	GAA	GAC	TGG	GAA	ATA	TTC	CGC	AAG	CTG	GGC	867
Gly	Lys	Ile	Ile	Glu	Val	Glu	Asp	Trp	Glu	Ile	Phe	Arg	Lys	Leu	Gly	
	270					275					280					
CTT	TAC	ATG	GCC	ACA	GTC	CTG	ACT	GGG	CTT	GCA	ATC	CAC	TCC	ATT	GTA	915
Leu	Tyr	Met	Ala	Thr	Val	Leu	Thr	Gly	Leu	Ala	Ile	His	Ser	Ile	Val	
285					290					295					300	
ATT	CTC	CCG	CTG	ATA	TAT	TTC	ATA	GTC	GTA	CGA	AAG	AAC	CCT	TTC	CGA	963
Ile	Leu	Pro	Leu	Ile	Tyr	Phe	Ile	Val	Val	Arg	Lys	Asn	Pro	Phe	Arg	
				305				310						315		
TTT	GCC	ATG	GGA	ATG	GCC	CAG	GCT	CTC	CTG	ACA	GCT	CTC	ATG	ATC	TCT	1011
Phe	Ala	Met	Gly	Met	Ala	Gln	Ala	Leu	Leu	Thr	Ala	Leu	Met	Ile	Ser	
			320					325					330			

TCC Ser	AGT Ser	TCA Ser 335	GCA Ala	ACA Thr	CTG Leu	CCT Pro	GTC Val 340	ACC Thr	TTC Phe	CGC Arg	TGT Cys	GCT Ala 345	GAA Glu	GAA Glu	AAT Asn	1059
AAC Asn 350	CAG Gln	GTG Val	GAC Asp	AAG Lys	AGG Arg	ATC Ile 355	ACT Thr	CGA Arg	TTC Phe	GTG Val	TTA Leu 360	CCC Pro	GTT Val	GGT Gly	GCA Ala	1107
ACA Thr 365	ATC Ile	AAC Asn	ATG Met	GAT Asp	GGG Gly 370	ACC Thr	GCG Ala	CTC Leu	TAT Tyr	GAA Glu 375	GCA Ala	GTG Val	GCA Ala	GCG Ala	GTG Val 380	1155
TTT Phe	ATT Ile	GCA Ala	CAG Gln	TTG Leu 385	AAT Asn	GAC Asp	CTG Leu	GAC Asp	TTG Leu 390	GGC Gly	ATT Ile	GGG Gly	CAG Gln	ATC Ile 395	ATC Ile	1203
ACC Thr	ATC Ile	AGT Ser 400	ATC Ile	ACG Thr	GCC Ala	ACA Thr	TCT Ser 405	GCC Ala	AGC Ser	ATC Ile	GGA Gly	GCT Ala 410	GCT Ala	GGC Gly	GTG Val	1251
CCC Pro	CAG Gln 415	GCT Ala	GGC Gly	CTG Leu	GTG Val	ACC Thr	ATG Met 420	GTG Val	ATT Ile	GTG Val	CTG Leu	AGT Ser 425	GCC Ala	GTG Val	GGC Gly	1299
CTG Leu 430	CCC Pro	GCC Ala	GAG Glu	GAT Asp	GTC Val	ACC Thr	CTG Leu 435	ATC Ile	ATT Ile	GCT Ala	GTC Val 440	GAC Asp	TGG Trp	CTC Leu	CTG Leu	1347
GAC Asp 445	CGG Arg	TTC Phe	AGG Arg	ACC Thr	ATG Met 450	GTC Val	AAC Asn	GTC Val	CTT Leu	GGT Gly 455	GAT Asp	GCT Ala	TTT Phe	GGG Gly	ACG Thr 460	1395
GGC Gly	ATT Ile	GTG Val	GAA Glu	AAG Lys 465	CTC Leu	TCC Ser	AAG Lys	AAG Lys	GAG Glu 470	CTG Leu	GAG Glu	CAG Gln	ATG Met	GAT Asp 475	GTT Val	1443
TCA Ser	TCT Ser	GAA Glu 480	GTC Val	AAC Asn	ATT Ile	GTG Val	AAT Asn	CCC Pro 485	TTT Phe	GCC Ala	TTG Leu	GAA Glu 490	TCC Ser	ACA Thr	ATC Ile	1491
CTT Leu	GAC Asp	AAC Asn 495	GAA Glu	GAC Asp	TCA Ser	GAC Asp	ACC Thr 500	AAG Lys	AAG Lys	TCT Ser	TAT Tyr	GTC Val 505	AAT Asn	GGA Gly	GGC Gly	1539
TTT Phe 510	GCA Ala	GTA Val	GAC Asp	AAG Lys	TCT Ser	GAC Asp 515	ACC Thr	ATC Ile	TCA Ser	TTC Phe	ACC Thr 520	CAG Gln	ACC Thr	TCA Ser	CAG Gln	1587
TTC Phe 525	TAGGGCCCCT GGCTGCAGAT GACTGGAAAC AAGGAAGGAC ATTTTCGTGAG															1640
AGTCATCTCA AACACGGCTT AAGGAAAAGA GAAA																1674

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 525 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Gly	Lys	Pro	Ala	Arg	Lys	Gly	Cys	Pro	Ser	Trp	Lys	Arg	Phe	Leu
1				5					10					15	
Lys	Asn	Asn	Trp	Val	Leu	Leu	Ser	Thr	Val	Ala	Ala	Val	Val	Leu	Gly
			20					25					30		
Ile	Thr	Thr	Gly	Val	Leu	Val	Arg	Glu	His	Ser	Asn	Leu	Ser	Thr	Leu
		35					40					45			
Glu	Lys	Phe	Tyr	Phe	Ala	Phe	Pro	Gly	Glu	Ile	Leu	Met	Arg	Met	Leu
	50					55					60				
Lys	Leu	Ile	Ile	Leu	Pro	Leu	Ile	Ile	Ser	Ser	Met	Ile	Thr	Gly	Val
65					70					75					80
Ala	Ala	Leu	Asp	Ser	Asn	Val	Ser	Gly	Lys	Ile	Gly	Leu	Arg	Ala	Val
				85					90					95	
Val	Tyr	Tyr	Phe	Cys	Thr	Thr	Leu	Ile	Ala	Val	Ile	Leu	Gly	Ile	Val
			100					105					110		
Leu	Val	Val	Ser	Ile	Lys	Pro	Gly	Val	Thr	Gln	Lys	Val	Gly	Glu	Ile
		115					120					125			
Ala	Arg	Thr	Gly	Ser	Thr	Pro	Glu	Val	Ser	Thr	Val	Asp	Ala	Met	Leu
	130					135					140				
Asp	Leu	Ile	Arg	Asn	Met	Phe	Pro	Glu	Asn	Leu	Val	Gln	Ala	Cys	Phe
145					150					155					160
Gln	Gln	Tyr	Lys	Thr	Lys	Arg	Glu	Glu	Val	Lys	Pro	Pro	Ser	Asp	Pro
				165					170					175	
Glu	Met	Asn	Met	Thr	Glu	Glu	Ser	Phe	Thr	Ala	Val	Met	Thr	Thr	Ala
			180					185					190		
Ile	Ser	Lys	Asn	Lys	Thr	Lys	Glu	Tyr	Lys	Ile	Val	Gly	Met	Tyr	Ser
		195					200					205			
Asp	Gly	Ile	Asn	Val	Leu	Gly	Leu	Ile	Val	Phe	Cys	Leu	Val	Phe	Gly
	210					215					220				
Leu	Val	Ile	Gly	Lys	Met	Gly	Glu	Lys	Gly	Gln	Ile	Leu	Val	Asp	Phe
225					230					235					240
Phe	Asn	Ala	Leu	Ser	Asp	Ala	Thr	Met	Lys	Ile	Val	Gln	Ile	Ile	Met
				245					250					255	
Cys	Tyr	Met	Pro	Leu	Gly	Ile	Leu	Phe	Leu	Ile	Ala	Gly	Lys	Ile	Ile
			260					265					270		
Glu	Val	Glu	Asp	Trp	Glu	Ile	Phe	Arg	Lys	Leu	Gly	Leu	Tyr	Met	Ala

275	280	285
Thr Val Leu Thr Gly Leu Ala Ile His Ser Ile Val Ile Leu Pro Leu		
290	295	300
Ile Tyr Phe Ile Val Val Arg Lys Asn Pro Phe Arg Phe Ala Met Gly		
305	310	315
Met Ala Gln Ala Leu Leu Thr Ala Leu Met Ile Ser Ser Ser Ser Ala		
	325	330
Thr Leu Pro Val Thr Phe Arg Cys Ala Glu Glu Asn Asn Gln Val Asp		
	340	345
Lys Arg Ile Thr Arg Phe Val Leu Pro Val Gly Ala Thr Ile Asn Met		
	355	360
Asp Gly Thr Ala Leu Tyr Glu Ala Val Ala Ala Val Phe Ile Ala Gln		
	370	375
Leu Asn Asp Leu Asp Leu Gly Ile Gly Gln Ile Ile Thr Ile Ser Ile		
	385	390
Thr Ala Thr Ser Ala Ser Ile Gly Ala Ala Gly Val Pro Gln Ala Gly		
	405	410
Leu Val Thr Met Val Ile Val Leu Ser Ala Val Gly Leu Pro Ala Glu		
	420	425
Asp Val Thr Leu Ile Ile Ala Val Asp Trp Leu Leu Asp Arg Phe Arg		
	435	440
Thr Met Val Asn Val Leu Gly Asp Ala Phe Gly Thr Gly Ile Val Glu		
	450	455
Lys Leu Ser Lys Lys Glu Leu Glu Gln Met Asp Val Ser Ser Glu Val		
	465	470
Asn Ile Val Asn Pro Phe Ala Leu Glu Ser Thr Ile Leu Asp Asn Glu		
	485	490
Asp Ser Asp Thr Lys Lys Ser Tyr Val Asn Gly Gly Phe Ala Val Asp		
	500	505
Lys Ser Asp Thr Ile Ser Phe Thr Gln Thr Ser Gln Phe		
	515	520
		525

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGGGTACC GCCATGGAGA AGAGCAAC

28

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCGTCTAGA TCACAGAACC GACTCCTTG

29

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCGGGTACC AATATGACTA AAAGCAATG

29

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGCGTCTAGA CTACATCTTG GTTTCCTG

29

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCGGGTACC ACCATGGCAT CTACGGAAG

29

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCGTCTAGA TTATTTCTCA CGTTTCCAAG

30

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 28 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCGGGTACC GCCATGGGGA AACCGGCG

28

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 28 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGCGGGATCC CTAGAACTGT GAGGTCTG

28